Listing of Claims:

This listing of claims replaces all prior versions, and listings, of claims in the captioned application.

1. (Original) A computer system comprising at least one database correlating the presence of at least one mutation in a human immunodeficiency virus (HIV) reverse transcriptase and a change in susceptibility of at least one strain of HIV to a reverse transcriptase inhibitor, comprising at least one record corresponding to a correlation between at least one mutation 194G in said reverse transcriptase, and treatment with at least a reverse transcriptase inhibitor.

2. (Original) A method for evaluating the effectiveness of a reverse transcriptase inhibitor as an antiviral therapy for a patient infected with at least one mutant HIV straincomprising:
   (i) collecting a sample from an HIV-infected patient;
   (ii) determining whether the sample comprises a nucleic acid encoding HIV reverse transcriptase having at least one mutation 194G;
   (iii) correlating the presence of said at least one mutation of step (ii) to a change in effectiveness of said reverse transcriptase inhibitor.

3. (Original) A method for identifying a drug effective against mutant HIV reverse transcriptase, comprising:
   (i) providing a HIV reverse transcriptase nucleic acid comprising at least one mutation 194G;
   (ii) recombining said nucleic acid of step (i) into a proviral nucleic acid deleted for said sequence to generate a recombinant HIV virus;
   (iii) determining a phenotypic response of said drug to said HIV reverse transcriptase; and
   (iv) identifying a drug effective against mutant HIV based on the phenotypic response of step (iii) .

4. (Original) A method for identifying a drug effective against mutant HIV reverse transcriptase, comprising:

(i) providing a HIV reverse transcriptase comprising at least one mutation 194G;
(ii) determining the activity of said drug on said HIV reverse transcriptase;
(iii) determining the activity of said drug on wild type HIV reverse transcriptase;
(iv) determining the ratio of the activity determined in step (iii) over the activity determined in step (ii);
(v) identifying an effective drug against mutant HIV based on the ratio of step (iv).

5. (Original) A method for evaluating a change in viral drug susceptibility comprising:
(i) collecting a sample from an HIV-infected patient;
(ii) determining whether the sample comprises a HIV reverse transcriptase having at least one mutation 194G;
(iii) correlating the presence of said at least one mutation of step (ii) to a change in viral drug susceptibility.

6. (Original) A method for evaluating a change in viral drug susceptibility, comprising:
(i) providing an HIV comprising a reverse transcriptase comprising at least one mutation 194G;
(ii) determining a phenotypic response of said virus to said drug; and
(iii) correlating the phenotypic response of step (ii) to a change in viral drug susceptibility.

7. (Original) A method for evaluating a change in drug effectiveness against mutant HIV reverse transcriptase, comprising:
(i) providing a HIV reverse transcriptase comprising at least one mutation 194G;
(ii) determining the activity of said drug on said reverse transciptase;
(iii) determining the activity of said drug on wild type HIV reverse transcriptase and;
(iv) determining the ratio of the activity determined in step (iii) over the activity determined in step (ii);

(v) identifying an effective drug against mutant HIV based on the ratio of step (iv).

8. (Original) A vector for performing phenotypic analysis comprising an HIV sequence having at least one mutation 194G in the HIV reverse transcriptase.

9. (Original) An isolated and purified HIV reverse transcriptase sequence having at least one mutation 194G, wherein said at least one mutation in said sequence correlates to a fold change in susceptibility towards a HIV reverse transcriptase inhibitor.

10. (Original) An isolated and purified oligonucleotide comprising a HIV reverse transcriptase sequence of 5 to 100 bases for in vitro diagnosis of viral drug resistance, characterized in that said oligonucleotide comprises at least one mutation 194G.